

SEQUENCE LISTING

<110> Gray, Kevin A.
Aboushadi, Nahla M.
Garrett, James B.

<120> Amylases, Nucleic Acids Encoding them and Methods For Making and Using them

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 Ser Lys Asp Cys Val Ser Ile Ser His Asn Leu Ile Val Lys Gln Leu
 85 90 95
 Ser Ile Ile Asn Lys Thr Asn Ser Glu Lys Asp Ile Lys Leu Phe Phe
 100 105 110
 Tyr Glu Asn Leu Arg Ile Gly Glu Thr Pro Ser Lys Ser Thr Val Lys
 115 120 125
 Phe Val Lys Glu Lys Asn Cys Leu Ile Lys His Asp Lys Asn Tyr Ile
 130 135 140
 Phe Cys Ile Gly Ser Asn Lys Lys Val Ser Ser Tyr Gln Cys Gly Ile
 145 150 155 160
 Lys Tyr Ser Glu Ser Ser Ala Leu Arg Asp Ile Glu Asn Gly Val Leu

165 170 175
 Lys Glu Gln Ser Ser Ala Thr Gly Leu Ile Thr Asp Ser Ala Leu Cys
 180 185 190
 Trp Glu Phe Lys Ile Lys Pro Asn Gln Lys Tyr Thr Leu Ser Ile Leu
 195 200 205
 Ile Leu Pro Glu Lys Tyr Asp Gly Asp Tyr Asn Lys Thr Leu Asn Leu
 210 215 220
 Met Asp Thr Leu His Met Val Lys Asp Asn Leu Lys Asp Leu Tyr Asn
 225 230 235 240
 Leu Thr Arg Asn Phe Trp Lys Ser Arg Val Asp Ser Met Val Asn Lys
 245 250 255
 Trp Gly Ile Leu Lys Leu Glu Glu Tyr Lys Glu Cys Ile Asp Ile Cys
 260 265 270
 Lys Arg Ser Leu Leu Thr Leu Leu Leu Leu Cys Asp Tyr Lys Gly Gly
 275 280 285
 Ile Ile Ala Ser Pro Ser Leu His Pro Asp Tyr Arg Tyr Val Trp Cys
 290 295 300
 Arg Asp Ala Gly Tyr Met Ala Val Ala Leu Asp Leu Cys Gly Gln His
 305 310 315 320
 Glu Met Ser Glu Lys Tyr Phe Glu Trp Cys Lys Thr Thr Gln Asn Ser
 325 330 335
 Asp Gly Ser Trp Val Gln Asn Tyr Tyr Val Glu Gly Tyr Pro Arg Phe
 340 345 350
 Thr Ala Ile Gln Ile Asp Gln Val Gly Thr Thr Ile Trp Ala Leu Leu
 355 360 365
 Val His Tyr Arg Ile Thr Gly Asp Lys His Phe Leu Lys Arg Asn Trp
 370 375 380
 Glu Met Val Lys Lys Ala Gly Asp Tyr Leu Ser Arg Ala Ala Asp Gln
 385 390 395 400
 Leu Ile Pro Cys Tyr Asp Leu Trp Glu Glu Lys Phe Gly Val Phe Ala
 405 410 415
 Tyr Thr Leu Gly Ala Ile Tyr Gly Gly Leu Lys Ser Gly Tyr Leu Ile
 420 425 430
 Gly Lys Glu Leu Asp Lys Glu Glu Glu Ile Gln His Trp Lys Lys Ser
 435 440 445
 Met Asn Phe Leu Lys Asn Glu Val Val Asn Arg Leu Tyr Leu Lys Asn
 450 455 460
 Glu Lys Arg Phe Ala Lys Ser Leu Lys Pro Leu Asp Lys Thr Ile Asp
 465 470 475 480
 Thr Ser Ile Leu Gly Leu Ser Phe Pro Tyr Gly Leu Val Ser Val Asp
 485 490 495
 Asp Pro Arg Ile Ile Ser Thr Ala Asn Gln Ile Glu Lys Ala Phe Asn
 500 505 510
 Tyr Lys Val Gly Gly Val Gly Arg Tyr Pro Glu Asp Ile Tyr Phe Gly
 515 520 525
 Gly Asn Pro Trp Ile Ile Thr Thr Leu Trp Leu Tyr Met Tyr Tyr Lys
 530 535 540
 Lys Leu Val Asp Thr Leu Ser Lys Lys Gly Lys Phe Gln Glu Ser Ile
 545 550 555 560
 Ile Asp Asn Tyr Asn Lys Lys Cys Tyr Asn Leu Leu Lys Trp Ile Leu
 565 570 575

Lys His Gln Phe Asn Gly Met Phe Pro Glu Gln Val His Lys Asp Leu
 580 585 590
 Gly Ile Pro Ile Ser Ala Ile Pro Leu Gly Trp Ser His Ala Met Val
 595 600 605
 Ile Ile Ala Ile His Gly Asp Tyr Asp Ile Leu Ile Pro
 610 615 620

<210> 9

> 1848

DNA

> Archaea

<210> 9

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 ggcag ttatgataa aaaagtaaag tggcatiggg atgatgatt ggatataacc 180
 aatatac ttgaggaaac gaacatattt aaaactatct tagaagatga taagattata 240
 accatta aagatttgt gccagtatct cacaacgtgc ttataagaag agtgtatata 300
 aataaataac tgataaaaa attaaattt aagctcttt ttacgaaaa ttgagaatt 360
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 aatggaaaat atatttttg cattggaagt gataaaagaa tagattcatt tcagtgtgga 480
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 aaagagagtt ctggattatt aaccgatagt gcaatatcat ggaatataaa gattgatgaa 600
 anaagaagtt tggcattcaa catctacata ctccacaaa gattcgatgg agattttca 660
 ataataactg aacaactaaa gattataatg aataacagtg aaaacattaa aaatctctca 720
 atgaattatt ggaaacatat tatagggag ataatagat ttatacatcc tgagcttagg 780
 caaataata agatttttc tataactaaa agggctttaa tgacacttt aatgttatgt 840
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<210> 10

<211> 615

<212> PRT

<213> Archaea

<400> 10

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 35 40 45
 Val Lys Trp His Trp Asp Asp Asp Trp Asp Ile Thr Gln Lys Tyr Ile
 50 55 60
 Glu Glu Thr Asn Ile Phe Lys Thr Ile Leu Glu Asp Asp Lys Ile Ile
 65 70 75 80
 Leu Thr Ile Lys Asp Phe Val Pro Val Ser His Asn Val Leu Ile Arg
 85 90 95
 Arg Val Tyr Ile Lys Asn Lys Leu Asp Lys Lys Leu Asn Phe Lys Leu
 100 105 110
 Phe Phe Tyr Glu Asn Leu Arg Ile Gly Glu Asn Pro Ile Thr Asn Thr
 115 120 125
 Val Lys Phe Leu Glu Asp Gly Cys Ile Val Lys Tyr Asn Gly Lys Tyr
 130 135 140
 Ile Phe Cys Ile Gly Ser Asp Lys Arg Ile Asp Ser Phe Gln Cys Gly
 145 150 155 160
 Asn Arg Tyr Ser Lys Thr Ser Ala Tyr Ile Asp Ile Glu Asn Gly Ile
 165 170 175
 Leu Lys Glu His Lys Glu Ser Ser Gly Leu Leu Thr Asp Ser Ala Ile
 180 185 190
 Ser Trp Asn Ile Lys Ile Asp Glu Lys Arg Ser Leu Ala Phe Asn Ile
 195 200 205
 Tyr Ile Leu Pro Gln Arg Phe Asp Gly Asp Phe Ser Ile Ile Thr Glu
 210 215 220
 Gln Leu Lys Ile Ile Met Asn Asn Ser Glu Asn Ile Lys Asn Leu Ser
 225 230 235 240
 Met Asn Tyr Trp Lys His Ile Ile Gly Glu Ile Asn Arg Phe Ile His
 245 250 255
 Pro Glu Leu Arg Gln Asn Asn Lys Ile Tyr Ser Ile Thr Lys Arg Ala
 260 265 270
 Leu Met Thr Leu Leu Met Leu Cys Asp Lys Glu Gly Gly Ile Ile Ala
 275 280 285
 Ala Pro Ser Leu His Pro Asp Tyr Arg Tyr Val Trp Gly Arg Asp Gly
 290 295 300
 Ser Tyr Ile Ser Ile Ala Leu Asp Leu Phe Gly Ile Arg Asn Ile Pro
 305 310 315 320
 Asp Arg Phe Phe Glu Phe Met Ser Lys Ile Gln Asn Ala Asp Gly Ser
 325 330 335
 Trp Leu Gln Asn Tyr Tyr Val Asn Gly Lys Pro Arg Leu Thr Ala Ile
 340 345 350
 Gln Thr Asp Gln Ile Gly Ser Ile Leu Trp Ala Met Asp Val His Tyr
 355 360 365
 Arg Leu Thr Gly Asp Arg Lys Phe Val Glu Arg Tyr Trp Asn Thr Ile
 370 375 380
 Glu Lys Ala Ala Asn Tyr Leu Arg Leu Val Ala Leu Asn Phe Thr Pro
 385 390 395 400
 Cys Phe Asp Leu Trp Glu Glu Arg Phe Gly Val Phe Ala Tyr Thr Met

405 410 415
 Gly Ala Thr Tyr Ala Gly Leu Lys Cys Ala Tyr Ser Met Ser Lys Ala
 420 425 430
 Val Asn Lys Arg Asp Lys Val Lys Asp Trp Gly Lys Thr Ile Glu Phe
 435 440 445
 Leu Lys His Glu Val Pro Lys Arg Phe Tyr Leu Glu Asp Glu Glu Arg
 450 455 460
 Phe Ala Lys Ser Ile Asn Pro Leu Asp Lys Thr Ile Asp Thr Ser Ile
 465 470 475 480
 Leu Gly Leu Ser Tyr Pro Phe Asn Leu Ile Asp Val Asp Asp Glu Arg
 485 490 495
 Met Ile Lys Thr Ala Glu Ala Ile Glu Lys Ala Phe Lys Tyr Lys Val
 500 505 510
 Gly Gly Ile Gly Arg Tyr Pro Glu Asp Ile Tyr Phe Gly Gly Asn Pro
 515 520 525
 Trp Ile Ile Thr Thr Leu Trp Leu Ser Leu Tyr Tyr Arg Arg Leu Tyr
 530 535 540
 Lys Val Leu Lys Glu Lys Asp Asp Asn Gly Ala Asp Ile Tyr Leu Gln
 545 550 555 560
 Lys Ser Lys Lys Leu Phe Asn Trp Val Met Lys Tyr Ser Phe Asp Gly
 565 570 575
 Leu Phe Pro Glu Gln Ile His Lys Glu Leu Gly Val Pro Met Ser Ala
 580 585 590
 Met Pro Leu Gly Trp Ser Asn Ala Met Phe Leu Ile Tyr Val Tyr Glu
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 Asn Asp Lys Val Ile Ile Pro
 610 615

<210> 11

<211> 2034

<212> DNA

<213> Archaea

<400> 11

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 tcatttgcca tattttatga taataagttg aaatggaatt gggacaattc ctgggatatt 180
 aatcagaact atttaaaaga tacaacata ttgaaaacat catatgaaaa cgaggatttt 240
 ctaatagaat caaaggacta cgtgcctata tcccataact cgataattaa gcaaatatca 300
 atattaaaca aatccagcga aaaaaagaat taaaactgt tttttatga aaatttaaga 360
 atgggagaaa ttctgaagt aagtactgta aagtatagaa agaacaggga gtgcattatt 420
 aaatacgata agaattatgt ttttgtatc ggcagtaata aaaaagtatc tcataccaa 480
 tgtggtgta ggtcatccga gagtagtgcc cttaatgatc tcaaaaatgg tattttaag 540
 gaatacgata gtgctgaagg cctaatacaca gatagcgcac tgggttgga ccttgagttg 600
 agtccaaatc aggaacagaa agtctcaata tttatattg cagataagta tgggtgggat 660
 tataacaaaa ttatgaattt attggataca ctaaatatag ttataaccaa tcacgcagac 720
 atatatgatc ttacaatggc atactggaag aacatgattg aaaccactgc gaatagtcta 780
 tgcaattcaa atcaagtctt taaagattta acacataata aagacgacgc aaatatttca 840
 aatttaaaaa gaataaaaca gtatgaagct atttgtaaaa gatccctatt aaccatttta 900
 ctcttttgat atcataatgg tgaataatt gcatcccat cactctatcc agattataga 960
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 gttcaaaact actacgtaga aggaaatcca aggcttacgg caattcaaat tgaccaagtt 1140
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 cacgatatcc aaaattggaa agagagcatg gacttcctta aaaacgaaat ggtagatagg 1440
 ctttatttaa aagatgaaaa tagatttga aaatcattgg atccattga caaagctcta 1500
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 catatgtact atgaaaactt gattaaatca ttatctaac atggtaaaaa tgccatacat 1740
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 gcccaaaaat gtaacaattt gtttgattgg actttaaagt ataacttaa tgaactatt 1920
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<210> 12

<211> 677

<212> PRT

<213> Archaea

<400> 12

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 35 40 45
 Lys Leu Lys Trp Asn Trp Asp Asn Ser Trp Asp Ile Asn Gln Asn Tyr
 50 55 60
 Leu Lys Asp Thr Asn Ile Leu Lys Thr Ser Tyr Glu Asn Glu Asp Phe
 65 70 75 80
 Leu Ile Glu Ser Lys Asp Tyr Val Pro Ile Ser His Asn Ser Ile Ile
 85 90 95
 Lys Gln Ile Ser Ile Leu Asn Lys Ser Ser Glu Lys Lys Asn Leu Lys
 100 105 110
 Leu Phe Phe Tyr Glu Asn Leu Arg Met Gly Glu Ile Pro Glu Val Ser
 115 120 125
 Thr Val Lys Tyr Arg Lys Asn Arg Glu Cys Ile Ile Lys Tyr Asp Lys
 130 135 140
 Asn Tyr Val Phe Cys Ile Gly Ser Asn Lys Lys Val Ser Ser Tyr Gln
 145 150 155 160
 Cys Gly Val Arg Ser Ser Glu Ser Ser Ala Leu Asn Asp Leu Lys Asn
 165 170 175
 Gly Ile Leu Lys Glu Tyr Asp Ser Ala Glu Gly Leu Ile Thr Asp Ser
 180 185 190
 Ala Leu Gly Trp Asp Leu Glu Leu Ser Pro Asn Gln Glu Gln Lys Val
 195 200 205
 Ser Ile Phe Ile Phe Ala Asp Lys Tyr Gly Gly Asp Tyr Thr Lys Ile

210 215 220
 Met Asn Leu Leu Asp Thr Leu Asn Ile Val Ile Thr Asn His Ala Asp
 225 230 235 240
 Ile Tyr Asp Leu Thr Met Ala Tyr Trp Lys Asn Met Ile Glu Thr Thr
 245 250 255
 Ala Asn Ser Leu Cys Asn Ser Asn Gln Val Phe Lys Asp Leu Thr His
 260 265 270
 Ile Lys Asp Asp Ala Asn Ile Ser Asn Leu Lys Arg Ile Lys Gln Tyr
 275 280 285
 Glu Ala Ile Cys Lys Arg Ser Leu Leu Thr Ile Leu Leu Leu Cys Asp
 290 295 300
 His Asn Gly Gly Ile Ile Ala Ser Pro Ser Leu Tyr Pro Asp Tyr Arg
 305 310 315 320
 Tyr Val Trp Cys Arg Asp Ala Gly Tyr Met Ala Val Ala Leu Asp Leu
 325 330 335
 Cys Gly Gln His Gly Ile Ser Glu Lys Tyr Phe Glu Trp Cys Lys Lys
 340 345 350
 Thr Gln Asn Ser Asp Gly Ser Trp Val Gln Asn Tyr Tyr Val Glu Gly
 355 360 365
 Asn Pro Arg Leu Thr Ala Ile Gln Ile Asp Gln Val Gly Thr Thr Ile
 370 375 380
 Trp Ala Ala Leu Val His Tyr Arg Ile Thr Arg Asp Lys Leu Phe Leu
 385 390 395 400
 Asn Arg Tyr Trp Glu Met Ile Lys Lys Ala Gly Asp Tyr Leu Ser Ser
 405 410 415
 Val Ala Asn Pro Pro Ser Pro Ser Tyr Asp Leu Trp Glu Glu Lys Tyr
 420 425 430
 Gly Val Phe Ala Tyr Thr Leu Gly Ala Ile Tyr Gly Gly Leu Lys Ser
 435 440 445
 Ala Tyr Asn Ile Cys Lys Ile Leu Gly Lys Glu Glu His Asp Ile Gln
 450 455 460
 Asn Trp Lys Glu Ser Met Asp Phe Leu Lys Asn Glu Met Val Asp Arg
 465 470 475 480
 Leu Tyr Leu Lys Asp Glu Asn Arg Phe Ala Lys Ser Leu Asp Pro Leu
 485 490 495
 Asp Lys Ala Leu Asp Ala Ser Ile Leu Gly Leu Ser Phe Pro Tyr Asn
 500 505 510
 Leu Val Pro Val Asp Asp Pro Arg Met Ile Ser Thr Ala Asn Gln Ile
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 Glu Asn Ala Phe Lys Tyr Lys Val Gly Gly Ile Gly Arg Tyr Pro Glu
 530 535 540
 Asp Val Tyr Phe Gly Gly Asn Pro Trp Ile Ile Thr Thr Ile Trp Leu
 545 550 555 560
 His Met Tyr Tyr Glu Asn Leu Ile Lys Ser Leu Ser Lys His Gly Lys
 565 570 575
 Asn Ala Ile His Ser Asp Gln Ile Pro Asp Ser Ser Gly Asp Leu Lys
 580 585 590
 Asp Phe Val Ser Ile Ile Gly Ser Ile Glu Asn His Gly Glu Lys Ser
 595 600 605
 Asp Glu Thr Pro Ser Ser Asp Thr Leu Leu Thr Tyr Ala Gln Lys Cys
 610 615 620

Asn Asn Leu Phe Asp Trp Thr Leu Lys Tyr Asn Phe Asn Glu Leu Phe
 625 630 635 640
 Pro Glu Gln Val His Lys Asp Leu Gly Ala Pro Ile Ser Ala Ile Pro
 645 650 655
 Leu Gly Trp Ser His Ala Met Val Ile Ile Ala Ile His Gly Asn Phe
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 Asp Ile Leu Ile Pro
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<210> 13

<211> 1779

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 13

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 gacactaata tattcaaaac tactttagaa aatgagaata tcatatttgt tataaaagat 240
 ttatgtccaa ttacacataa tgtattaatt aggagagttt tcattaaaaa taaactcca 300
 tataattata attttaaact atttttctat gaaaatctta gaattggaga acatccttca 360
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 tgtataagca gtgataaaaa aataaattca tatcagtgtg gaaatagata tagtgaaaaa 480
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 ctaactgaca gtgctattga atgggatata gatttaaaac cacatggaaa agtagcattt 600
 aacatctaca tcttctctca tattggaaat aatatagaga ttataaaaaa tcagttaaatt 660
 attattaaaa atctctcttc tgaataaaaa aatatatctc taaattattg gaagagttct 720
 ttgatataa aaggttatct atttaatgaa aatatattaa aattagcaaa aagggtctta 780
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 cctgattata gatatgtttg gggtagagat ggaagtata tggctgtggc attatccatt 900
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 tatactttag gagcaatgta tggaggatta agggcaggat gtagttagc taaagctata 1260
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 aaaaagctat ttaattgggt tattaacct atctatctat tcctgaaca gatacataaa 1680
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<210> 14

<211> 592

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 14

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      35           40           45
Lys Glu Trp Ser Val Tyr Gln Lys Tyr Ile Glu Asp Thr Asn Ile
      55           60
Lys Thr Thr Leu Glu Asn Glu Asn Ile Ile Phe Val Ile Lys Asp
      70           75           80
Leu Val Pro Ile Ser His Asn Val Leu Ile Arg Arg Val Phe Ile Lys
      85           90           95
Asn Lys Leu Pro Tyr Asn Tyr Asn Phe Lys Leu Phe Phe Tyr Glu Asn
      100          105          110
Leu Arg Ile Gly Glu His Pro Ser Glu Asn Thr Val Lys Phe Leu Asp
      115          120          125
Asp Cys Ile Val Lys Phe Asn Gly Lys Tyr Thr Phe Cys Ile Ser Ser
      130          135          140
Asp Lys Lys Ile Asn Ser Tyr Gln Cys Gly Asn Arg Tyr Ser Glu Lys
      145          150          155          160
Ser Ala Tyr Lys Asp Ile Glu Asn Gly Leu Leu Ser Glu Asn Pro Glu
      165          170          175
Ser Val Gly Val Leu Thr Asp Ser Ala Ile Glu Trp Asp Ile Asp Leu
      180          185          190
Lys Pro His Gly Lys Val Ala Phe Asn Ile Tyr Ile Phe Pro His Ile
      195          200          205
Gly Asn Asn Ile Glu Ile Ile Lys Asn Gln Leu Asn Ile Ile Lys Asn
      210          215          220
Leu Ser Ser Glu Ile Lys Asn Ile Ser Leu Asn Tyr Trp Lys Ser Ser
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Phe Asp Ile Lys Gly Tyr Leu Phe Asn Glu Lys Tyr Leu Lys Leu Ala
      245          250          255
Lys Arg Ala Leu Met Ile Leu Thr Met Leu Ser Asp Lys Asn Gly Gly
      260          265          270
Ile Ile Ala Ser Pro Ser Ile His Pro Asp Tyr Arg Tyr Val Trp Gly
      275          280          285
Arg Asp Gly Ser Tyr Met Ala Val Ala Leu Ser Ile Tyr Gly Ile Lys
      290          295          300
Asn Ile Pro Trp Arg Phe Phe His Phe Met Ser Lys Val Gln Asn Leu
      305          310          315          320
Asp Gly Ser Trp Leu Gln Asn Tyr Tyr Thr Asp Gly Lys Pro Arg Leu
      325          330          335
Thr Ala Leu Gln Ile Asp Gln Ile Gly Ser Val Leu Trp Ala Met Glu
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Val Tyr Tyr Arg Thr Thr Gly Asp Arg Glu Phe Val Lys Lys Phe Trp
 355 360 365
 Glu Thr Ile Glu Lys Ala Gly Asn Phe Leu Tyr Asn Ala Ser Leu Ser
 370 375 380
 Leu Met Pro Cys Phe Asp Leu Trp Glu Glu Lys Tyr Gly Val Phe Ser
 385 390 395 400
 Tyr Thr Leu Gly Ala Met Tyr Gly Gly Leu Arg Ala Gly Cys Ser Leu
 405 410 415
 Ala Lys Ala Ile Glu Glu Lys Lys Glu Asp Trp Lys Lys Ala Leu Asp
 420 425 430
 Lys Leu Lys Lys Asp Val Asp Leu Leu Tyr Leu Ser Asp Glu Glu Arg
 435 440 445
 Phe Val Lys Ser Ile Asn Pro Leu Asn Lys Glu Ile Asp Thr Ser Ile
 450 455 460
 Leu Gly Leu Ser Tyr Pro Phe Gly Leu Val Lys Val Asn Asp Glu Arg
 465 470 475 480
 Met Ile Lys Thr Ala Glu Ala Ile Glu Lys Ala Phe Lys Tyr Lys Val
 485 490 495
 Gly Gly Ile Gly Arg Tyr Pro Ser Asp Val Tyr Phe Gly Gly Asn Pro
 500 505 510
 Trp Ile Ile Thr Thr Leu Trp Leu Ala Leu Tyr Tyr Arg Arg Leu Phe
 515 520 525
 Ile Thr Thr Asn Asp Arg Lys Tyr Leu Glu Lys Ser Lys Lys Leu Phe
 530 535 540
 Asn Trp Val Ile Asn His Ile Tyr Leu Phe Pro Glu Gln Ile His Lys
 545 550 555 560
 Glu Leu Ala Ile Pro Val Ser Ala Met Pro Leu Gly Trp Ser Cys Ala
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 Met Leu Leu Phe Tyr Leu Tyr Lys Asn Asp Asp Ile Ile Val Ile Lys
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<210> 15

<211> 2121

<212> DNA

<213> Bacterial

<400> 15

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 caagcagtaa atggccctgg agaggctgat acttgggcta aagctcagaa acaaggtgta 180
 gggactgcaa acaactatac ttccaaagta tggttacca ttgcagacgg ggggatatct 240
 gaggttact atccgactat agatactgct gatgtaaagg atattaaatt tttgtgaca 300
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 actgaaaaat cgttgggcta taaaatcatt aacacagata aagaaggag atataagata 420
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